

Laser-aligned molecular-beam diffraction for proteins. Serial Crystallography

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The possibility of obtaining X-ray diffraction patterns from a beam of hydrated proteins which are aligned by a laser beam is discussed. This "serial crystallography" method uses the non-linear effect of the RMS electric field from a CW fiber laser on the non-resonant electronic polarizability for alignment. The laser beam crosses a steady beam of proteins within a jet of vitreous iceballs. The rotational recoil of the iceballs, dissipation mechanisms and the conditions of temperature and laser power needed for a given degree of alignment and resolution will be discussed. Exposure times at the ALS, and charge-density reconstruction methods are briefly outlined with the aim of seeing secondary structure in proteins which cannot be crystallized". For details, see PRL 92,198102 (2004)